

CLAIMS

WE CLAIM:

1. An isolated nucleic acid molecule having a polymorphic site and comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-22
5 and the complements thereof.
2. An isolated nucleic acid molecule comprising a portion of a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-22 and the complements thereof which is at least 10 nucleotides in length and comprises a polymorphic site.
- 10 3. An isolated nucleic acid molecule according to Claim 1, wherein the nucleotide at the polymorphic site is different from the nucleotide at the polymorphic site in a corresponding reference allele.
4. An isolated allele-specific oligonucleotide which hybridizes to a nucleic acid molecule having a polymorphic site and comprising a nucleic acid sequence
15 selected from the group consisting of SEQ ID NOS: 1-22 and the complements thereof under high stringency conditions.
5. An isolated allele-specific oligonucleotide according to Claim 4, which is at least 10 nucleotides in length.
- 20 6. An isolated allele-specific oligonucleotide according to Claim 4, in which a nucleotide occupying a central position of said oligonucleotide aligns with and is complementary to a nucleotide occupying the polymorphic site of the nucleic acid molecule to which it hybridizes.

7. An isolated allele-specific oligonucleotide according to Claim 4, in which a nucleotide occupying the 3' end of said oligonucleotide aligns with and is complementary to a nucleotide occupying the polymorphic site of the nucleic acid molecule to which it hybridizes.
- 5 8. An isolated peptide encoded by a nucleic acid molecule according to Claim 1.
9. A method of analyzing a nucleic acid sample for polymorphisms, comprising the steps of:
 - 10 (a) obtaining a nucleic acid sample from one or more individuals, and
 - (b) determining the nucleotide occupying one or more of the polymorphic sites of one or more nucleic acid molecules selected from the group consisting of SEQ ID NOS: 1-22.
10. A method according to Claim 9, wherein the nucleic acid sample is obtained from a plurality of individuals, and the nucleotide occupying one or more of the polymorphic sites is determined in each of the individuals.
- 15 11. A method according to Claim 9, further comprising testing each individual for the presence of a disease phenotype and correlating the presence of the disease phenotype with the nucleotide present at one or more polymorphic sites.
12. A method for predicting the likelihood that an individual will have a cardiovascular disease, comprising the steps of:
 - 20 (a) obtaining a nucleic acid sample from an individual to be assessed; and
 - (b) determining the nucleotide present at a polymorphic site of one or more nucleic acid molecules having a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1-22,

wherein the presence of a nucleotide associated with a lower likelihood of having a cardiovascular disease indicates that the individual has a lower likelihood of having a cardiovascular disease than if another nucleotide was present at the polymorphic site.

- 5 13. A method according to Claim 12, wherein the cardiovascular disease is coronary heart disease.

14. A method for predicting the likelihood that an individual will have a cardiovascular disease, comprising the steps of:

- 10 (a) obtaining a nucleic acid sample from an individual to be assessed; and
 (b) determining the nucleotide present at a polymorphic site of one or more nucleic acid molecules having a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1-22,

- 15 wherein the presence of a nucleotide associated with a greater likelihood of having a cardiovascular disease indicates that the individual has a greater likelihood of having a cardiovascular disease than if another nucleotide was present at the polymorphic site.

15. A method according to Claim 14, wherein the cardiovascular disease is coronary heart disease.